

Replace the paragraph beginning at page 18, line 12, with the following rewritten paragraph:

C3 SUB 34
Figure 7 depicts the cDNA sequence of human LIG46 (SEQ ID NO:13).

Replace the paragraph beginning at page 18, line 13, with the following rewritten paragraph:

C4
Figure 8 depicts the predicted amino acid sequence of human LIG46 (SEQ ID NO:14).

Replace the paragraph beginning at page 18, line 15, with the following rewritten paragraph:

C5
Figure 9 depicts an alignment of the cDNA sequences of human LIG46 (upper sequence; SEQ ID NO:13) and murine LIG46 (lower sequence; SEQ ID NO:1).

Replace the paragraph beginning at page 18, line 18, with the following rewritten paragraph:

C6
Figure 10 depicts an alignment of the predicted amino acid sequences of human LIG46 (upper sequence; SEQ ID NO:14) and murine LIG46 (lower sequence; SEQ ID NO:2).

Replace the paragraph beginning at page 19, line 20, with the following rewritten paragraph:

C7 SUB
~~A nucleotide sequence encoding murine LIG56 protein is shown in Figure 4 (SEQ ID NO:4; SEQ ID NO:6 includes the open reading frame only). A predicted amino acid sequence of LIG46 protein is also shown in Figure 4 (SEQ ID NO:5).~~

Replace the paragraph beginning at page 19, line 24, with the following rewritten paragraph:

CS
~~The murine LIG56 cDNA of Figure 4 (SEQ ID NO:6) encodes a 400 amino acid protein.~~

Replace the paragraph beginning at page 93, line 15, with the following rewritten paragraph:

C7
The LIG46 cDNA isolated as described above (SEQ ID NO:1) has a 1191 nucleotide open reading frame (SEQ ID NO:3) which encodes a 397 amino acid protein (SEQ ID NO:2). This protein includes a predicted signal sequence of about 32 amino acids (from amino acid 1 to about amino acid 32 of SEQ ID NO:2) and a predicted mature protein of about 365 amino acids (from about amino acid 33 to amino acid 397 of SEQ ID NO:2; SEQ ID NO:4). The extracellular domain of LIG46 extends from about amino acid 33 to about amino acid 302. LIG46 protein possesses one predicted transmembrane domain which extends from about amino acid 303 (extracellular end) to about 320 (intracellular end) of SEQ ID NO:2. The cytoplasmic domain of LIG46 extends from about amino acid 321 to about amino acid 397.

Replace the paragraph beginning at page 94, line 18, with the following rewritten paragraph:

Portions of LIG46 are similar to certain galactosyltransferases. Figure 2 depicts a series of alignments of portions of the amino acid sequence of LIG46 (SEQ ID NO:2) with portions of a number of galactosyltransferases, including: *Mus musculus* UDP-Gal: betaGlcNAc beta 1,3-galactosyltransferase-I (Accession Number AF029790; SEQ ID NO:8); *Mus musculus* IPP-Gal: betaGlcNAc beta 1,3-galactosyltransferase-III (Accession Number AF029792; SEQ ID NO:9); *Drosophila melanogaster* neurogenic secreted signalling protein (Accession Number U41449;

SWB
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SEQ ID NO:10); and *Homo sapiens* UDP-galactose: 2-acetamido-2-deoxy-D-glucose 3beta-galactosyltransferase (Accession Number Y15014; SEQ ID NO:11). A majority sequence is depicted above the solid line (SEQ ID NO:12). Conserved residues are shaded. These residues are more likely conserved in functional variants of LIG46.

Replace the paragraph beginning at page 95, line 5, with the following rewritten paragraph:

SWB
Full

Figure 7 depicts the cDNA sequence of a full-length human LIG46 clone. Figure 8 depicts the predicted amino acid sequence of human LIG46. The human LIG46 cDNA depicted in Figure 7 (SEQ ID NO:13) has a 1191 nucleotide open reading frame which encodes a 397 amino acid protein (SEQ ID NO:14). This protein includes a predicted signal sequence of about 32 amino acids (from amino acid 1 to about amino acid 32 of SEQ ID NO:14) and a predicted mature protein of about 365 amino acids (from about amino acid 33 to amino acid 397 of SEQ ID NO:14; SEQ ID NO:15). Figure 9 depicts an alignment of the cDNA sequences of human LIG46 (upper sequence) and murine LIG46 (lower sequence). Figure 10 depicts an alignment of the predicted amino acid sequences of human LIG46 (upper sequence) and murine LIG46 (lower sequence).

Replace the paragraph beginning at page 96, line 6, with the following rewritten paragraph:

Briefly, the LIG46 gene was mapped using the Genebridge 4 Radiation Hybrid panel. A pair of primers within the 3' untranslated region of LIG46 (forward-CCATGTTGGGGTCTCACATTAGAG, SEQ ID NO:18; and reverse-GGTAAGTCAGACCAATATCCTGCC, SEQ ID NO:19) were used to amplify DNA from the Genebridge 4 panel. The PCR products were run on a 2% agarose gel, stained with SYBR Gold and scanned. Linkage analysis was performed using the Map Manager QT623 software package.

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Replace the paragraph beginning at page 98, line 12, with the following rewritten paragraph:

For this study, a phosphothioate-protected antisense oligodeoxynucleotide and its respective control sequence (sense) were synthesized. The antisense oligodeoxynucleotide targets the LIG46 start codon mRNA at position 39.

Antisense: 5' CTT CGA CGC CCC ACA CTC AT 3' (SEQ ID NO:16)

Sense: 5' ATG AGT GTG GGG CGT CGA AG 3' (SEQ ID NO:17)

13
Male obese *ob/ob* C57BL/6J (45 g) mice were individually housed in macrolon cages (22±2° C; 12:12 h light/dark cycle with lights off at 6 pm). Tap water and mouse chow diet were given *ad libitum*. Mice were stereotactically implanted with a chronic guide cannula aimed to the third ventricle (intracerebroventricular) one week prior to this experiment.